



Figure 1A

1 GGAAGTCAGCAGCGTTGGGAGGGGTGCCGGGGGAATAGCGGGCAGC
51 AGCCCCAGCCCTCAGAGACAGCAGAAAGGAGGGAGGGTGCTGG
101 GGGGACAGCCCCCACCATTCTTACCCTATGGGCCCAACCTCCCACTCC
151 CACCTCCCCCTCATCGGCCGGGCTAGGACACCCCCCAATCCCCGTCGCCC
201 CCTTGGCACCGACACCCCCGACAGACAGAGACACAGCCATCCGCCACCA
251 CCGCTGCCGAGCCTGGCTGGGAGGGGCCAGCCCCCAGGCCCTAC
301 CCCTCTGAGGTGCCAGA ATG GAT TTG TGG CCA GGG GCA TGG
Met Asp Leu Trp Pro Gly Ala Trp
343 ATG CTG CTG CTG CTC TTC CTG CTG CTG CTC TTC C
Met Leu Leu Leu Leu Phe Leu Leu Leu Phe L
20
10
380 TG CTG CCC ACC CTG TGG TTC TGC AGC CCC AGT GCC AAG
eu Leu Pro Thr Leu Trp Phe Cys Ser Pro Ser Ala Lys
30

Figure 1 B

418 TAC TTC TTC AAG ATG GCC TTC TAC AAT GGC TGG ATC C
Tyr Phe Phe Lys Met Ala Phe Tyr Asn Gly Trp Ile L

40

455 TC TTC CTG GCT GTG CTC GCC ATC CCT GTG TGT GCC GTG
eu Phe Leu Ala Val Leu Ala Ile Pro Val Cys Ala Val

50

493 CGA GGA CGC AAC GTC GAG AAC ATG AAG ATC TTG CGT C
Arg Gly Arg Asn Val Glu Asn Met Lys Ile Leu Arg L

70

60

530 TA ATG CTG CTC CAC ATC AAA TAC CTG TAC GGG ATC CGA
eu Met Leu Leu His Ile Lys Tyr Leu Tyr Gly Ile Arg

80

Figure 1C

568 GTG GAG GTG CGA GGG GCT CAC CAC TTC CCT CCC TCG C
Val Glu Val Arg Gly Ala His His Phe Pro Pro Ser G

90

605 AG CCC TAT GTT GTT GTC TCC AAC CAC CAG AGC TCT CTC
In Pro Tyr Val Val Val Ser Asn His Gln Ser Ser Leu

100

643 GAT CTG CTT GGG ATG ATG GAG GTA CTG CCA GGC CGC T
Asp Leu Leu Gly Met Met Glu Val Leu Pro Gly Arg C

120

110

680 GT GTG CCC ATT GCC AAG CGC GAG CTA CTG TGG GCT GGC
ys Val Pro Ile Ala Lys Arg Glu Leu Leu Trp Ala Gly

130

Figure 1D

718 TCT GCC GGG CTG GCC TGC TGG CTG GCA GGA GTC ATC T
Ser Ala Gly Leu Ala Cys Trp Leu Ala Gly Val Ile P

140

755 TC ATC GAC CGG AAG CGC ACG GGG GAT GCC ATC AGT GTC
he Ile Asp Arg Lys Arg Thr Gly Asp Ala Ile Ser Val

150

793 ATG TCT GAG GTC GCC CAG ACC CTG CTC ACC CAG GAC G
Met Ser Glu Val Ala Gln Thr Leu Leu Thr Gln Asp V

170

160

830 TG AGG GTC TGG GTG TTT CCT GAG GGA ACG AGA AAC CAC
al Arg Val Trp Val Phe Pro Glu Gly Thr Arg Asn His

180

Figure 1E

868 AAT GGC TCC ATG CTG CCC TTC AAA CGT GGC GCC TTC C
Asn Gly Ser Met Leu Pro Phe Lys Arg Gly Ala Phe H

190

905 AT CTT GCA GTG CAG GCC CAG GTT CCC ATT GTC CCC ATA
is Leu Ala Val Gln Ala Gln Val Pro Ile Val Pro Ile

200

943 GTC ATG TCC TCC TAC CAA GAC TTC TAC TGC AAG AAG G
Val Met Ser Ser Tyr Gln Asp Phe Tyr Cys Lys Lys G

220

210

980 AG CGT CGC TTC ACC TCG GGA CAA TGT CAG GTG CGG GTG
lu Arg Arg Phe Thr Ser Gly Gln Cys Gln Val Arg Val

230

Figure 1F

1018 CTG CCC CCA GTG CCC ACG GAA GGG CTG ACA CCA GAT G
Leu Pro Pro Val Pro Thr Glu Gly Leu Thr Pro Asp A

240

1055 AC GTC CCA GCT CTG GCT GAC AGA GTC CGG CAC TCC ATG
sp Val Pro Ala Leu Ala Asp Arg Val Arg His Ser Met

250

1093 CTC ACT GTT TTC CGG GAA ATC TCC ACT GAT GGC CGG G
Leu Thr Val Phe Arg Glu Ile Ser Thr Asp Gly Arg G

270

260

1130 GT GGT GGT GAC TAT CTG AAG AAG CCT GGG GGC GGT GGG
ly Gly Gly Asp Tyr Leu Lys Lys Pro Gly Gly Gly 280

1168 TGA ACCCTGGCTCTGAGCTCTCCTCCCATCTGTCCCCATCTTCTCCCC

1216 CACACCTACCCACCCAGTGGGCCCTGAGCAGGGCCAAACCCTCTTCTCTT

1266 GTCTCCCCCTCTCCCCACTTATTCTCCTCTTTGGAATCTTCAACTTCTGAA

Figure 1G

1316 GTGAATGTGGATACAGGCCACTCCTGCCCCCTCTTGGCCCCCATCCATGG
1366 ACTCTTGCCCTCGGTGCAGTTTCCACTCTTGACCCCCACCTCCTACTGTCT
1416 TGTCTGTGGACAGTTGCCCTCCCCCTCATCTCCAGTGACTCAGCCCTACAC
1466 AAGGAGGGGAACATTCCATCCCCAGTGGAGTCTCTCCTATGTGTCTT
1516 CTCTACCCCTCTACCCCCACATTGGCCAGTGGACTCATCCATTCTTTGGA
1566 ACAAAATCCCCCCCACCTCCAAGTCCATGGATTCAATGGACTCATCCATT
1616 TGTGAGGAGGACTTCTCGCCCTCTGGCTGGAAGCTGATACCTGAAGCACT
1666 CCCAGGCTCATCCTGGGAGCTTTCCTCAGCACCTTCACCTTCCCCTCCCAG
1716 TGTAGCCTCCTGTCAGTGGGGGCTGGACCCCTTCTAATTCAGAGTCTCAT
1766 GCCTGCCCTTGCCCAGATGCCCCAGGGTCGTGCACTCTCTGGGATACCAGT
1816 TCAGTCTCCACATTTCTGGTTTCTGTGTCCCCCATAGTACAGTTCTTCAGTG
1866 GACATGACCCCAACCAGCCCCCTGCAGCCCTGCTGACCATCTCACCAGAC
1916 ACAAGGGGAAGAAGCAGACATCAGGTGCTGCACTCACTTCTGCCCCCTGG
1966 GGAGTTGGGAAAGGAACCAACCCCTGGCTGGAGGGGATAGGAGGCTTTT

Figure 1H

2016 AATTATTCTTTTCTGTTGAGGCTTCCCCCTCTCTGAGCCAGTTTTC
2066 TTTCTTCCGTGGTCATTAGCCACTCCCTGCCCTCTCACTCCAGACCTGTT
2116 CCCACAAC TGGGAGGTAGGCTGGGAGCAAAAGGAGAGGGTGGGACCCAG
2166 TTTTGGCGTGGTTGGTTTATTATTAATCTGGATAACAGCAAAAAAACTG
2216 AAAATAAAGAGAGAGAGAAAAA

Figure 2 A

Human LPAAT	1	MDLWPGAWM-	10	20	30	40	50
Yeast LPAAT	1	MSV-IGRFLY	YLRSVL-VVL	AL-AG-----	LL-LLELLPT	LWFCSPSAKY	F-----FKMA
E.coli LPAAT	1	M-----	LYIF	RL-IITVIYS	ILVCVFGSIY	-----	-----G
Maize LPAAT	1	MAI-----	PLVLVVL	PLGLLFLLSG	LIVNAIQAVL	FVTIRPFSSKS	-----
Human LPAAT	51	FYNGWILFLA	VLAIPVCAVR	GRNVENMKIL	RLMLLHIKYL	-YGIRVEVRG	-----
Yeast LPAAT	51	FY-----G	VIASILCTLI	GKQHLAQWIT	ARCFYHVMKL	MLGLDV---K	-----
E.coli LPAAT	51	-----	CLFS	PRNPKHVATF	GHMFGRLAPL	-FGLKVECRK	-----
Maize LPAAT	51	FYRRINRFLA	EL-----	-----L	WLQLVWVVDW	WAGVKVQLHA	-----
Human LPAAT	101	AHFE-PPSQ-	PYVVVSNHQ	SSLDLLGMME	VL--PGRC--	-VPI-AKREL	-----
Yeast LPAAT	101	VUGE-ENLAK	KPYIMIANHQ	STLDIFMLGR	IF--PPGCT-	---VTAKKSL	-----
E.coli LPAAT	101	PTDA-ESYG-	NAIYIANHQ	NNYDMVTASN	IVQ-PP----	TVTIV-GKKSL	-----
Maize LPAAT	101	DEETYRSMGK	EHALIISNHR	SDIDWL-IGW	ILAQRSGCLG	STLAVMKKSS	-----
Human LPAAT	151	LWAGSAGLAC	W---LAGVIF	IDRKRTGDAL	SVMSEVAQTL	LTQDVRVWV-	-----
Yeast LPAAT	151	KYVPFLG---	WFMAISGTYF	LDRSKRQEI	DTLNKGLENV	KKNKRALWV-	-----
E.coli LPAAT	151	LWIPFFGQLY	W---LTGNLL	IDRNNRTKAH	GTIAEVVNHF	KKRRI SIWM-	-----
Maize LPAAT	151	KFLPVIGWSM	WF---AEYLF	LEERS-WAKDE	KTLKWGLQRL	KDFPRPFWLA	-----
Human LPAAT	201	FPEGTRNHN	GS-----	-----	MLPFKRGAFH	LAVQAQVPIV	-----
Yeast LPAAT	201	FPEGTRSYT	SEL-----	-----T	MLPFKKGAFH	LAQQGKIPIV	-----
E.coli LPAAT	201	FPEGTRSRG	RGL-----	-----	-LPFKTGAFH	AAIAAGVPPI	-----
Maize LPAAT	201	LFVEGTRFTP	AKLLAAQEYA	ASQGLPAPRN	VLIPTKGFV	SAVSIMRDFV	-----

Figure 2 B

Human LPAAT	251	<u>P</u> <u>I</u> <u>V</u> <u>M</u> <u>S</u> <u>S</u> <u>Y</u> <u>Q</u> <u>D</u> <u>F</u>	<u>Y</u> <u>C</u> <u>K</u> <u>K</u> <u>E</u> <u>R</u> <u>R</u> <u>F</u> <u>T</u> <u>S</u>	<u>G</u> <u>Q</u> <u>C</u> <u>Q</u> <u>V</u> <u>R</u> <u>V</u> <u>L</u> <u>P</u> <u>P</u>	<u>V</u> <u>P</u> <u>T</u> <u>E</u> <u>G</u> <u>L</u> <u>T</u> <u>P</u> <u>D</u> <u>D</u>	<u>V</u> <u>P</u> <u>A</u> <u>L</u> <u>A</u> <u>D</u> <u>R</u>
Yeast LPAAT	251	<u>P</u> <u>V</u> <u>V</u> <u>S</u> <u>N</u> <u>T</u> <u>S</u> <u>T</u> <u>L</u>	<u>V</u> <u>S</u> <u>P</u> <u>K</u> <u>Y</u> <u>G</u> <u>V</u> <u>F</u> <u>N</u> <u>R</u>	<u>G</u> <u>C</u> <u>M</u> <u>I</u> <u>V</u> <u>R</u> <u>I</u> <u>L</u> <u>K</u> <u>P</u>	<u>I</u> <u>S</u> <u>T</u> <u>E</u> <u>N</u> <u>L</u> <u>T</u> <u>K</u> <u>D</u> <u>K</u>	<u>I</u> <u>G</u> <u>E</u> <u>F</u> <u>A</u> <u>E</u> <u>K</u>
E.coli LPAAT	251	<u>P</u> <u>V</u> <u>C</u> <u>V</u> <u>S</u> <u>T</u> <u>T</u> <u>S</u> <u>N</u> <u>K</u>	<u>I</u> <u>--</u> <u>N</u> <u>L</u> <u>N</u> <u>R</u> <u>L</u> <u>H</u> <u>N</u>	<u>G</u> <u>L</u> <u>V</u> <u>I</u> <u>V</u> <u>E</u> <u>M</u> <u>L</u> <u>P</u> <u>P</u>	<u>I</u> <u>D</u> <u>V</u> <u>S</u> <u>Q</u> <u>Y</u> <u>G</u> <u>K</u> <u>D</u> <u>Q</u>	<u>V</u> <u>R</u> <u>E</u> <u>L</u> <u>A</u> <u>A</u> <u>H</u>
Maize LPAAT	251	<u>P</u> <u>A</u> <u>I</u> <u>Y</u> <u>D</u> <u>T</u> <u>--</u> <u>V</u>	<u>I</u> <u>V</u> <u>P</u> <u>K</u> <u>D</u> <u>S</u> <u>P</u> <u>Q</u> <u>P</u> <u>T</u>	<u>M</u> <u>L</u> <u>R</u> <u>I</u> <u>L</u> <u>K</u> <u>G</u> <u>Q</u> <u>S</u> <u>S</u>	<u>V</u> <u>I</u> <u>H</u> <u>V</u> <u>R</u> <u>M</u> <u>K</u> <u>R</u> <u>H</u> <u>A</u>	<u>M</u> <u>S</u> <u>E</u> <u>M</u> <u>P</u> <u>K</u> <u>S</u> <u>D</u> <u>E</u> <u>D</u>
		310	320	330	340	350
Human LPAAT	301	-----	<u>V</u> <u>R</u> <u>H</u> <u>S</u> <u>M</u> <u>L</u> <u>T</u> <u>V</u> <u>-</u> <u>F</u>	<u>R</u> <u>E</u> <u>I</u> <u>S</u> <u>T</u> <u>D</u> <u>G</u> <u>R</u> <u>G</u> <u>G</u>	<u>G</u> <u>D</u> <u>Y</u> <u>L</u> <u>K</u> <u>K</u> <u>P</u> <u>G</u> <u>G</u> <u>G</u>	<u>G</u> <u>*</u>
Yeast LPAAT	301	-----	<u>V</u> <u>R</u> <u>D</u> <u>Q</u> <u>M</u> <u>V</u> <u>D</u> <u>T</u> <u>-</u> <u>L</u>	<u>K</u> <u>E</u> <u>I</u> <u>G</u> <u>Y</u> <u>S</u> <u>P</u> <u>A</u> <u>I</u> <u>N</u>	<u>D</u> <u>T</u> <u>T</u> <u>L</u> <u>P</u> <u>P</u> <u>Q</u> <u>--</u>	-----
E.coli LPAAT	301	-----	<u>C</u> <u>R</u> <u>S</u> <u>I</u> <u>M</u> <u>E</u> <u>Q</u> <u>K</u> <u>-</u> <u>I</u>	<u>A</u> <u>E</u> <u>L</u> <u>D</u> <u>K</u> <u>E</u> <u>V</u> <u>A</u> <u>E</u> <u>-</u>	-----	<u>R</u> <u>E</u> <u>A</u> <u>A</u> <u>G</u> <u>K</u> <u>V</u> <u>*</u>
Maize LPAAT	301	<u>V</u> <u>S</u> <u>K</u> <u>W</u> <u>C</u> <u>K</u> <u>D</u> <u>I</u> <u>F</u> <u>V</u>	<u>A</u> <u>K</u> <u>D</u> <u>A</u> <u>L</u> <u>L</u> <u>D</u> <u>K</u> <u>H</u> <u>L</u>	<u>A</u> <u>T</u> <u>G</u> <u>T</u> <u>F</u> <u>D</u> <u>E</u> <u>E</u> <u>I</u> <u>R</u>	<u>P</u> <u>I</u> <u>G</u> <u>R</u> <u>P</u> <u>V</u> <u>K</u> <u>S</u> <u>L</u> <u>L</u>	<u>V</u> <u>T</u> <u>L</u> <u>F</u> <u>W</u> <u>S</u> <u>C</u> <u>L</u> <u>L</u> <u>L</u>
		360	370	380	390	400
Human LPAAT	351
Yeast LPAAT	351	-- <u>A</u> <u>I</u> <u>E</u> <u>Y</u> -- <u>A</u>	<u>A</u> <u>L</u> ----- <u>Q</u>	<u>H</u> <u>D</u> <u>K</u> <u>V</u> <u>N</u> <u>K</u> <u>K</u> <u>I</u> <u>K</u>	<u>N</u> <u>E</u> <u>P</u> <u>V</u> <u>P</u> <u>S</u> <u>V</u> <u>S</u> <u>I</u> <u>S</u>	<u>N</u> <u>D</u> <u>V</u> <u>N</u> <u>T</u> <u>H</u> <u>N</u> <u>E</u> <u>G</u> <u>S</u>
E.coli LPAAT	351
Maize LPAAT	351	<u>F</u> <u>G</u> <u>A</u> <u>I</u> <u>E</u> <u>F</u> <u>F</u> <u>K</u> <u>W</u> <u>T</u>	<u>Q</u> <u>L</u> <u>L</u> <u>S</u> <u>T</u> <u>W</u> <u>R</u> <u>G</u> <u>V</u> <u>A</u>	<u>F</u> <u>T</u> <u>A</u> <u>G</u> <u>M</u> <u>A</u> <u>L</u> <u>V</u> <u>T</u>	<u>G</u> <u>V</u> <u>M</u> <u>H</u> <u>V</u> <u>F</u> <u>I</u> <u>M</u> <u>F</u> <u>S</u>	<u>Q</u> <u>A</u> ----- <u>E</u> <u>R</u> <u>S</u>
		410	420	430	440	450
Human LPAAT	401
Yeast LPAAT	401	<u>S</u> ----- <u>V</u>	<u>K</u> <u>K</u> <u>M</u> <u>H</u> <u>*</u>
E.coli LPAAT	401
Maize LPAAT	401	<u>S</u> <u>S</u> <u>A</u> <u>R</u> <u>A</u> <u>A</u> <u>R</u> <u>N</u> <u>R</u> <u>V</u>	<u>K</u> <u>K</u> <u>E</u> <u>*</u>

Figure 3A

10	20	30	40	50	60
GGAGCGAGCT	GGCGGCGCCG	TCGGGCGCCG	GGCCGGGCCA	TGGAGCTGTG	GCCGTGTCTG
70	80	90	100	110	120
GGCGGCGGC	TGCTGTTGCT	GCTGCTGCTG	GTGCAGCTGA	GCCGCGCGGC	CGAGTTCTAC
130	140	150	160	170	180
GCCAAGGTGC	CCCTGTACTG	CGCGCTGTGC	TTCACGGTGT	CCGCCGTGGC	CTCGCTCGTC
190	200	210	220	230	240
TGCCTGCTGT	GCCACGGCGG	CCGGACGGTG	GAGAACATGA	GCATCATCGG	CTGGTTCTGTG
250	260	270	280	290	300
CGAAGCTTCA	AGTACTTTTA	CGGGCTCCGC	TTCGAGGTGC	GGGACCCGCG	CAGGCTGCAG
310	320	330	340	350	360
GAGGCCCGTC	CCTGTGTTCAT	CGTCTCCAAC	CACCAGAGCA	TCCTGGACAT	GATGGGCCCTC
370	380	390	400	410	420
ATGGAGGTCC	TTCCGGAGCG	CTGCGTGCAG	ATCGCCAAGC	GGGAGCTGCT	CTTCCTGGGG
430	440	450	460	470	480
CCCGTGGGCC	TCATCATGTA	CCTCGGGGGC	GTCCTTCTTCA	TCAACCGGCA	GCGCTCTAGC
490	500	510	520	530	540
ACTGCCATGA	CAGTGATGGC	CGACCTGGGC	GAGCGCATGG	TCAGGGAGAA	CCTCAAAGTG

Figure 3B

550	560	570	580	590	600
TGGATCTATC	CCGAGGGTAC	TCGCAACGAC	AATGGGGACC	TGCTGCCCTTT	TAAGAAGGGC
610	620	630	640	650	660
GCCTTCTACC	TGGCAGTCCA	GGCACAGGTG	CCCATCGTCC	CCGTGGTGTA	CTCTTCCTTC
670	680	690	700	710	720
TCCTCCTTCT	ACAACACCAA	GAAGAAAGTTC	TTCACCTTCAG	GAACAGTCCAC	AGTGCAGGTG
730	740	750	760	770	780
CTGGAAGCCA	TCCCCACCAG	CGGCCTCACT	GCGGCGGACG	TCCCTGGGCT	CGTGGACACC
790	800	810	820	830	840
TGCCACCGGG	CCATGAGGAC	CACCTTCCTC	CACATCTCCA	AGACCCCCCA	GGAGAACGGG
850	860	870	880	890	900
GCCACTGCGG	GGTCTGGCGT	GCAGCCGGCC	CAGTAGCCCA	GACCACGGCA	GGGCATGACC
910	920	930	940	950	960
TGGGGAGGGC	AGGTGGAAGC	CGATGGCTGG	AGGATGGGCA	GAGGGACTC	CTCCCCGGCTT
970	980	990	1000	1010	1020
CCAAATACCA	CTCTGTCCGG	CTCCCCCAGC	TCTCACTCAG	CCCCGGAAGC	AGGAAGCCCC
1030	1040	1050	1060	1070	1080
TTCTGTCACT	GGTCTCAGAC	ACAGGCCCTT	GGTGTCCCCCT	GCAGGGGGCT	CAGCTGGACC

Figure 3C

1090	1100	1110	1120	1130	1140
CTCCCCGGC	TCGAGGCAG	GGA CTGCGC	CCACGGCACC	TCTGGGNGCT	GGGNTGATAA
1150	1160	1170	1180	1190	1200
AGATGAGGCT	TGCGGCTGTG	GCCCGCTGGT	GGGCTGAGCC	ACAAGGCCCC	CGATGGCCCCA
1210	1220	1230	1240	1250	1260
GGAGCAGATG	GGAGGACCCC	GAGGCCAGGA	GTCCCAGACT	CACGCACCCCT	GGGCCACAGG
1270	1280	1290	1300	1310	1320
GAGCCGGGAA	TCGGGGCCCTG	CTGCTCCTGC	TGGCCTGAAG	AATCTGTGGG	GTCAGCAGCTG
1330	1340	1350	1360	1370	1380
TACTCCGTTG	CTGTTTTTTT	ATAAACACAC	TCTTGGA AAA	AAAAAAA AAA	AAAAAAA AAA
1390	1400	1410	1420	1430	1440
AAA.....

Figure 4 A

10	20	30	40	50
GGAGCGAGCTGGCGCGCGTGGCGCGCGCGCGGCC	ATG	GAG	CTG	TGG CCG
	Met	Glu	Leu	Trp Pro
60	70	80	90	
TGT CTG GCC GCG GCG CTG CTG TTG CTG CTG CTG	CTG	GAG	CTG	CAG CTG
Cys Leu Ala Ala	Leu Leu Leu Leu	Val Gln	Leu	20
100	110	120	130	140
AGC CGC GCG GCC GAG TTC TAC GCC AAG GTC GCC	CTG	TAC	TGC	GCG
Ser Arg Ala Ala	Glu Phe Tyr Ala Lys	Val Ala	Leu Tyr	Cys Ala
				30
150	160	170	180	
CTG TGC TTC ACG GTG TCC GCC GTG GCC TCG CTC	GTC	TGC	CTG	CTG
Leu Cys Phe Thr	Val Ser Ala Val Ala	Ser Leu	Val Cys	Leu
				50
190	200	210	220	230
TGC CAC GGC GGC CCG ACG GTG GAG AAC ATG AGC	ATC	ATC	ATC	GGC TGG
Cys His Gly Gly	Arg Thr Val Glu	Asn Met	Ser Ile	Gly Trp
				60

Figure 4B

240	TTC GTG CGA AGC TTC AAG TAC TTT TAC GGG CTC CGC TTC GAG GTG	250	260	270
	Phe Val Arg Ser Phe Lys Tyr Phe Tyr Gly Leu Arg Phe Glu Val	280	290	300
				310
				320
				330
				340
				350
				360
				370
				380
				390
				400
				410
				420
				430
				440
				450
				460
				470
				480
				490
				500
				510

TTC GTG CGA AGC TTC AAG TAC TTT TAC GGG CTC CGC TTC GAG GTG
Phe Val Arg Ser Phe Lys Tyr Phe Tyr Gly Leu Arg Phe Glu Val 80

280 290 300 310 320
CGG GAC CCG CGC AGG CTG CAG GAG GCC CGT CCC TGT GTC ATC GTC
Arg Asp Pro Arg Arg Leu Gln Glu Ala Arg Pro Cys Val Ile Val 90

330 340 350 360 370 380 390 400 410
TCC AAC CAC CAG AGC ATC CTG GAC ATG ATG GGC CTC ATG GAG GTC
Ser Asn His Gln Ser Ile Leu Asp Met Met Gly Leu Met Glu Val 110

370 380 390 400 410
CTT CCG GAG CGC TGC GTG CAG ATC GCC AAG CGG GAG CTC TTC
Leu Pro Glu Arg Cys Val Gln Ile Ala Lys Arg Glu Leu Phe 120

420 430 440 450
CTG GGG CCC GTG GGC CTC ATC ATG TAC CTC GGG GGC GTC TTC TTC
Leu Gly Pro Val Gly Leu Ile Met Tyr Leu Gly Gly Val Phe 140

460 470 480 490 500
ATC AAC CCG CAG CGC TCT AGC ACT GCC ATG ACA GTG ATG GCC GAC
Ile Asn Arg Gln Arg Ser Thr Ala Met Thr Val Met Ala Asp 150

Figure 4C

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510   CTG GGC GAG CGC ATG GTC AGG GAG AAC CTC AAA GTG TGG ATC TAT
      Leu Gly Glu Arg Met Val Arg Glu Asn Leu Lys Val Trp Ile Tyr
      160
520
530
540
550   CCC GAG GGT ACT CGC AAC GAC AAT GGG GAC CTG CTG CCT TTT AAG
      Pro Glu Gly Thr Arg Asn Asp Asn Gly Asp Leu Leu Pro Phe Lys
      180
560
570
580
590
600   AAG GGC GCC TTC TAC CTG GCA GTC CAG GCA CAG GTG CCC ATC GTC
      Lys Gly Ala Phe Tyr Leu Ala Val Gln Ala Gln Val Pro Ile Val
      190
610
620
630
640   CCC GTG GTG TAC TCT TCC TTC TCC TCC TTC TAC AAC ACC AAG AAG
      Pro Val Val Tyr Ser Ser Phe Ser Ser Phe Tyr Asn Thr Lys Lys
      210
650
660
670
680
690   AAG TTC TTC ACT TCA GGA ACA GTC ACA GTG CAG GTG CTG GAA GCC
      Lys Phe Phe Thr Ser Gly Thr Val Thr Val Gln Val Leu Glu Ala
      220
700
710
720
730
```


[illegible]

Figure 4E

1110	1120	1130	1140	1150	1160
	GGACTCGCGCC	CACGGCACCTCTGGNGCTGGNTGATAA	GATGAGGCTTGC	GGCTGTG	
1170	1180	1190	1200	1210	1220
	GCCCGCTGGTGGCTGAGCCACAAGCCCCCGATGGCC	CAGGAGCAGATGGGAGGACCCC			
1230	1240	1250	1260	1270	1280
	GAGGCCAGGAGTCCCAGACTCACGCACCCCTGGGCC	CACAGGAGCCGGGAATC	GGGGCCTG		
1290	1300	1310	1320	1330	1340
	CTGCTCCTGCTGGCCTGAAGAACTCTGTGGGT	CAGCACTGTACTCCGTTGCTTTTTTTT			
1350	1360	1370	1380		
	ATAAACACACTCTTGGAAAA	AAAAAAAAAAAAAAAAAAAA			

Figure 5 A

Alignment of LPAAT Sequences.

	10	20	30	40	50
Human LPAAT- β	1	---	---	MEL WPC	LA AALLLLLV
Human LPAAT- α	1	---	---	MDL WPGAWMLLL	IFLLFLFP
Yeast LPAAT	1	---	---	MSV	IGRFLYYL RSVLWLALA
E.coli LPAAT	1	---	---	---	---
H.influenzae	1	---	---	---	---
S.typhimurium	1	---	---	---	---
L.douglasi	1	MAKIRSS-L RNR	---	RQLKP AVAATAD	--D DKDGVFV--
C. nucifera	1	MDASCASSFL RCRCLESCFK ASFGMSQPKD	AAGQPSRRPA	DADDFIVDD	
Human LPAAT- β	51	QL---	SRAAE FYAKVAL-YC ALQFTVSAVA	SLVCLLCHGG	RTVENM-SII
Human LPAAT- α	51	TLWFCSRSK YFFKMAF-YN GWILFLAVLA	IPVCAV--RG	RNVENM-KIL	
Yeast LPAAT	51	G---CG---	FY-----GVIA	SIILTLICKQ	HIAQWI-TAR
E.coli LPAAT	51	---	MLYI	FRILITIVYS ILVC---	VFG SIYCLFSPRN PKHV---ATF
H.influenzae	51	---	MLKL	LRIFLMLICC ILIC---	VLG TIYSFIREKN PSNV---GIV
S.typhimurium	51	---	MLYI	FRILITIVYS ILVC---	VFG SIYCLFSPRN PKHV---ATF
L.douglasi	51	---	LLSC	FKIFVCFEFT VLIITAVANG	LIMLILPWP YMRIRGNLY
C. nucifera	51	DRWITVILSV VRIACFL--	SMWTTIVN	MIMLILPWP	YARIRGNLY

Figure 5 B

	110	120	130	140	150
Human LPAAT- β	101 <u>GMFVRSFKY</u> - --FYGLRFEV <u>RDPRLQEAR</u> <u>PCVIVSNHQ</u> <u>ILDMGLMEV</u>				
Human LPAAT- α	101 <u>RLMLIHICY</u> - --LYGIRVEV <u>RGAHFFPSQ</u> <u>PVWVSNHQ</u> <u>SLDILGMMEV</u>				
Yeast LPAAT	101 <u>CFY-HVMKL</u> - --MLGLDVKV <u>VGEENAK-K</u> <u>PYIMIANHQ</u> <u>TLDIFMLGRI</u>				
E.coli LPAAT	101 <u>GHMFGRL</u> --- <u>APLFLGLKVEC</u> <u>RKPTDAESYG</u> <u>NAIYIANHQ</u> <u>NYDMVTA SNI</u>				
H.influenzae	101 <u>ARWFGRL-FT</u> <u>YPLFLGLKVEH</u> <u>RIPQDQKQIS</u> <u>RAIYIGNHQ</u> <u>NYDMVT ISYM</u>				
S.typhimurii	101 <u>GHMFGRL-FT</u> <u>APLFLGLKVEC</u> <u>RKPADAENYG</u> <u>NAIYIANHQ</u> <u>NYDMVTAANI</u>				
L.douglassi	101 <u>GHIIGGLV</u> -- <u>IWIYGIPIKI</u> <u>QGSEHIKKRA</u> <u>IFTYISNHAS</u> <u>PIDAFVFMWL</u>				
C. nucifera	101 <u>GHVTGRMLFT</u> <u>MWILGNPITI</u> <u>EGSEFSNTRA</u> <u>I--YIQNHAS</u> <u>LVDIFLIMWL</u>				
	160	170	180	190	200
Human LPAAT- β	151 <u>LPERCVOIAK</u> <u>RELLFLGPV</u> - <u>GLIMVLGV</u> <u>FFINRQSSST</u> <u>AMT--VMALL</u>				
Human LPAAT- α	151 <u>LPGRCPPIAK</u> <u>RELLWAGSA</u> - <u>GLACWLAGV</u> <u>IFIDRKRTGD</u> <u>AIS--VMSEV</u>				
Yeast LPAAT	151 <u>FPPGCTVTAK</u> <u>KSLKVWFFL</u> - <u>GWFMALSGT</u> <u>YFLDRSKRQE</u> <u>AID--TINKG</u>				
E.coli LPAAT	151 <u>VQPPTVTGCK</u> <u>KSLWIWIPFF</u> - <u>GQLYWLTCN</u> <u>LLIDRNNRTK</u> <u>AHG--TIAEV</u>				
H.influenzae	151 <u>VQPRIVSVCK</u> <u>KSLWIWIPFF</u> <u>TGILYWVTGN</u> <u>IFLDRENRTK</u> <u>AHN--TMSQL</u>				
S.typhimurii	151 <u>VQPPTVTGCK</u> <u>KSLWIWIPFF</u> <u>TGQLYWLTCN</u> <u>LLIDRNNRAK</u> <u>AHS--TIAAV</u>				
L.douglassi	151 <u>APIGTGVAK</u> <u>KEVIWYPILG</u> <u>Q--LYTLAH</u> <u>IRIDRSNPAA</u> <u>AIQSFTMKEA</u>				
C. nucifera	151 <u>IPKGTVTIAK</u> <u>KEIIWYPLEG</u> <u>QFTLYVLANH</u> <u>QRIDRSNPFA</u> <u>AIES--IKEV</u>				

Figure 5C

	210	220	230	240	250		
Human LPAAT-β	201	<u>GERM</u> <u>REN</u> <u>LK</u>	<u>VW</u> <u>I</u> <u>Y</u> <u>PE</u> <u>G</u> <u>T</u> <u>R</u> <u>N</u>	<u>D</u> <u>N</u> <u>G</u> <u>D</u> <u>L</u> — <u>L</u> <u>P</u> <u>F</u>	<u>K</u> <u>K</u> <u>G</u> <u>A</u> <u>F</u> <u>Y</u> <u>L</u> — <u>A</u>	<u>V</u> <u>O</u> <u>A</u> <u>Q</u> <u>V</u> <u>P</u> <u>I</u> <u>V</u> <u>P</u> <u>V</u>	
Human LPAAT-α	201	<u>AQ</u> <u>T</u> <u>L</u> <u>L</u> <u>T</u> <u>Q</u> <u>D</u> <u>V</u> <u>R</u>	<u>VW</u> <u>V</u> <u>F</u> <u>P</u> <u>E</u> <u>G</u> <u>T</u> <u>R</u> <u>N</u>	<u>H</u> <u>N</u> <u>G</u> <u>S</u> <u>M</u> — <u>L</u> <u>P</u> <u>F</u>	<u>K</u> <u>R</u> <u>G</u> <u>A</u> <u>F</u> <u>H</u> <u>L</u> — <u>A</u>	<u>V</u> <u>O</u> <u>A</u> <u>Q</u> <u>V</u> <u>P</u> <u>I</u> <u>V</u> <u>P</u> <u>I</u>	
Yeast LPAAT	201	<u>LEN</u> <u>V</u> <u>K</u> <u>K</u> <u>N</u> <u>K</u> <u>R</u> <u>A</u>	<u>LW</u> <u>V</u> <u>F</u> <u>P</u> <u>E</u> <u>G</u> <u>T</u> <u>R</u> <u>S</u>	<u>Y</u> <u>T</u> <u>S</u> <u>E</u> <u>L</u> <u>T</u> <u>M</u> <u>L</u> <u>P</u> <u>F</u>	<u>K</u> <u>K</u> <u>G</u> <u>A</u> <u>F</u> <u>H</u> <u>L</u> — <u>A</u>	<u>Q</u> <u>Q</u> <u>G</u> <u>I</u> <u>P</u> <u>I</u> <u>V</u> <u>P</u> <u>V</u>	
E.coli LPAAT	201	<u>VN</u> <u>H</u> <u>F</u> <u>K</u> <u>K</u> <u>R</u> <u>R</u> <u>I</u> <u>S</u>	<u>IW</u> <u>M</u> <u>F</u> <u>P</u> <u>E</u> <u>G</u> <u>T</u> <u>R</u> <u>S</u>	<u>R</u> <u>G</u> <u>R</u> <u>G</u> <u>L</u> — <u>L</u> <u>P</u> <u>F</u>	<u>K</u> <u>T</u> <u>G</u> <u>A</u> <u>F</u> — <u>H</u> <u>A</u> <u>A</u>	<u>I</u> <u>A</u> <u>A</u> <u>G</u> <u>V</u> <u>P</u> <u>I</u> <u>I</u> <u>P</u> <u>V</u>	
H.influenzae	201	<u>ARR</u> <u>I</u> <u>N</u> <u>E</u> <u>D</u> <u>N</u> <u>L</u> <u>S</u>	<u>IW</u> <u>M</u> <u>F</u> <u>P</u> <u>E</u> <u>G</u> <u>T</u> <u>R</u> <u>N</u>	<u>R</u> <u>G</u> <u>R</u> <u>G</u> <u>L</u> — <u>L</u> <u>P</u> <u>F</u>	<u>K</u> <u>T</u> <u>G</u> <u>A</u> <u>F</u> <u>T</u> <u>F</u> <u>H</u> <u>A</u> <u>A</u>	<u>I</u> <u>S</u> <u>A</u> <u>G</u> <u>V</u> <u>P</u> <u>I</u> <u>I</u> <u>P</u> <u>V</u>	
S.typhimurii	201	<u>VN</u> <u>H</u> <u>F</u> <u>K</u> <u>K</u> <u>R</u> <u>R</u> <u>I</u> <u>S</u>	<u>IW</u> <u>M</u> <u>F</u> <u>P</u> <u>E</u> <u>G</u> <u>T</u> <u>R</u> <u>S</u>	<u>R</u> <u>G</u> <u>R</u> <u>G</u> <u>L</u> — <u>L</u> <u>P</u> <u>F</u>	<u>K</u> <u>T</u> <u>G</u> <u>A</u> <u>F</u> <u>T</u> <u>F</u> <u>H</u> <u>A</u> <u>A</u>	<u>I</u> <u>A</u> <u>A</u> <u>G</u> <u>V</u> <u>P</u> <u>I</u> <u>I</u> <u>P</u> <u>V</u>	
L.douglassi	201	<u>VR</u> <u>V</u> <u>I</u> <u>T</u> <u>E</u> <u>K</u> <u>N</u> <u>L</u> <u>S</u>	<u>L</u> <u>I</u> <u>M</u> <u>F</u> <u>P</u> <u>E</u> <u>G</u> <u>T</u> <u>R</u> <u>S</u>	<u>G</u> <u>D</u> <u>G</u> <u>R</u> <u>L</u> — <u>L</u> <u>P</u> <u>F</u>	<u>K</u> <u>K</u> <u>G</u> <u>F</u> <u>V</u> <u>H</u> <u>L</u> — <u>A</u>	<u>L</u> <u>Q</u> <u>S</u> <u>H</u> <u>L</u> <u>P</u> <u>I</u> <u>V</u> <u>P</u> <u>M</u>	
C. nucifera	201	<u>AR</u> <u>AW</u> <u>K</u> <u>K</u> <u>N</u> <u>L</u> <u>S</u>	<u>L</u> <u>I</u> <u>I</u> <u>F</u> <u>P</u> <u>E</u> <u>G</u> <u>T</u> <u>R</u> <u>S</u>	<u>K</u> <u>T</u> <u>G</u> <u>R</u> <u>L</u> — <u>L</u> <u>P</u> <u>F</u>	<u>K</u> <u>K</u> <u>G</u> <u>F</u> <u>T</u> <u>H</u> <u>F</u> <u>T</u> <u>I</u> <u>A</u>	<u>L</u> <u>Q</u> <u>I</u> <u>R</u> <u>L</u> <u>P</u> <u>I</u> <u>V</u> <u>P</u> <u>M</u>	
	260	270	280	290	300		
Human LPAAT-β	251	<u>VY</u> <u>S</u> <u>S</u> <u>F</u> <u>S</u> <u>S</u> — <u>F</u>	<u>Y</u> <u>N</u> <u>T</u> <u>K</u> <u>K</u> <u>F</u> <u>F</u> <u>T</u> <u>S</u>	<u>G</u> <u>T</u> <u>V</u> <u>I</u> <u>V</u> <u>Q</u> <u>V</u> <u>L</u> <u>E</u> <u>A</u>	<u>I</u> <u>P</u> <u>T</u> <u>S</u> <u>G</u> <u>L</u> <u>T</u> <u>A</u> <u>A</u> <u>D</u>	<u>V</u> <u>P</u> <u>A</u> <u>L</u> <u>V</u> <u>D</u> <u>T</u> <u>C</u> <u>H</u> <u>R</u>	
Human LPAAT-α	251	<u>VM</u> <u>S</u> <u>S</u> <u>Y</u> <u>Q</u> <u>D</u> — <u>F</u>	<u>Y</u> <u>C</u> <u>K</u> <u>K</u> <u>E</u> <u>R</u> <u>R</u> <u>F</u> <u>T</u> <u>S</u>	<u>G</u> <u>Q</u> <u>Q</u> <u>V</u> <u>R</u> <u>V</u> <u>L</u> <u>P</u> <u>P</u>	<u>V</u> <u>P</u> <u>T</u> <u>E</u> <u>G</u> <u>L</u> <u>T</u> <u>P</u> <u>D</u> <u>D</u>	<u>V</u> <u>P</u> <u>A</u> <u>L</u> <u>A</u> <u>D</u> <u>R</u> <u>V</u> <u>R</u> <u>H</u>	
Yeast LPAAT	251	<u>VV</u> <u>S</u> <u>N</u> <u>I</u> <u>S</u> <u>T</u> — <u>L</u>	<u>V</u> <u>S</u> <u>P</u> <u>K</u> <u>Y</u> <u>G</u> <u>V</u> <u>F</u> <u>N</u> <u>R</u>	<u>G</u> <u>C</u> <u>M</u> <u>I</u> <u>V</u> <u>R</u> <u>I</u> <u>L</u> <u>K</u> <u>P</u>	<u>I</u> <u>S</u> <u>T</u> <u>E</u> <u>N</u> <u>L</u> <u>T</u> <u>K</u> <u>D</u> <u>K</u>	<u>I</u> <u>G</u> <u>E</u> <u>F</u> <u>A</u> <u>E</u> <u>K</u> <u>V</u> <u>R</u> <u>D</u>	
E.coli LPAAT	251	<u>CV</u> <u>S</u> <u>T</u> <u>T</u> <u>S</u> —	<u>N</u> <u>K</u>	<u>I</u> <u>N</u> <u>L</u> <u>N</u> <u>R</u> <u>I</u> <u>H</u> <u>N</u>	<u>G</u> <u>L</u> <u>V</u> <u>I</u> <u>V</u> <u>E</u> <u>M</u> <u>L</u> <u>P</u> <u>P</u>	<u>I</u> <u>D</u> <u>V</u> <u>S</u> <u>Q</u> <u>G</u> <u>K</u> <u>D</u> <u>Q</u>	<u>V</u> <u>R</u> <u>E</u> <u>L</u> <u>A</u> <u>A</u> <u>H</u> <u>C</u> <u>R</u> —
H.influenzae	251	<u>V</u> <u>C</u> <u>S</u> <u>S</u> <u>T</u> <u>H</u> —	<u>N</u> <u>K</u>	<u>I</u> <u>N</u> <u>L</u> <u>N</u> <u>R</u> <u>W</u> <u>D</u> <u>N</u>	<u>G</u> <u>K</u> <u>V</u> <u>I</u> <u>C</u> <u>E</u> <u>I</u> <u>M</u> <u>D</u> <u>P</u>	<u>I</u> <u>D</u> <u>V</u> <u>S</u> <u>G</u> <u>Y</u> <u>T</u> <u>K</u> <u>D</u> <u>N</u>	<u>V</u> <u>R</u> <u>D</u> <u>L</u> <u>A</u> <u>A</u> <u>Y</u> <u>C</u> <u>H</u> <u>F</u>
S.typhimurii	251	<u>CV</u> <u>S</u> <u>N</u> <u>I</u> <u>S</u> —	<u>N</u> <u>K</u>	<u>V</u> <u>N</u> <u>L</u> <u>N</u> <u>R</u> <u>I</u> <u>N</u> <u>N</u>	<u>G</u> <u>L</u> <u>V</u> <u>I</u> <u>V</u> <u>E</u> <u>M</u> <u>L</u> <u>P</u> <u>P</u>	<u>V</u> <u>D</u> <u>V</u> <u>S</u> <u>E</u> <u>X</u> <u>G</u> <u>K</u> <u>D</u> <u>Q</u>	<u>V</u> <u>R</u> <u>E</u> <u>L</u> <u>A</u> <u>A</u> <u>H</u> <u>C</u> <u>R</u> <u>F</u>
L.douglassi	251	<u>I</u> <u>L</u> <u>T</u> <u>G</u> <u>T</u> <u>H</u> <u>L</u> <u>A</u> <u>W</u> <u>F</u>	<u>T</u> <u>R</u> <u>K</u> <u>G</u> <u>I</u> <u>F</u> <u>R</u> <u>V</u> <u>R</u> <u>P</u>	<u>V</u> <u>P</u> <u>I</u> <u>T</u> <u>V</u> <u>K</u> <u>Y</u> <u>L</u> <u>P</u> <u>P</u>	<u>I</u> <u>N</u> <u>T</u> <u>D</u> <u>D</u> <u>W</u> <u>T</u> <u>V</u> <u>D</u> <u>K</u>	<u>I</u> <u>D</u> <u>D</u> <u>V</u> <u>K</u> <u>M</u> <u>I</u> <u>H</u> <u>D</u>	
C. nucifera	251	<u>V</u> <u>L</u> <u>T</u> <u>G</u> <u>T</u> <u>H</u> <u>L</u> <u>A</u> <u>W</u> —	<u>R</u> <u>K</u> <u>N</u> <u>S</u> <u>L</u> <u>R</u> <u>V</u> <u>R</u> <u>P</u>	<u>A</u> <u>P</u> <u>I</u> <u>T</u> <u>V</u> <u>K</u> <u>Y</u> <u>F</u> <u>S</u> <u>P</u>	<u>I</u> <u>K</u> <u>T</u> <u>D</u> <u>D</u> <u>W</u> <u>E</u> <u>E</u> <u>E</u> <u>K</u>	<u>I</u> <u>N</u> <u>H</u> <u>Y</u> <u>V</u> <u>E</u> <u>M</u> <u>I</u> <u>H</u> <u>F</u>	

Figure 5D

	310	320	330	340	350
Human LPAAT-β	301	AMRTTFIHIS	KTFQENGATA	GSGVQPAQ*	-----
Human LPAAT-α	301	SMLTVFREIS	TDGRGGDYL	KPGGGG*	-----
Yeast LPAAT	301	QMVDILKEIG	YSPAINDTTL	PFQAIEYAAL	QHDKKVKKI KNEPVPSVSI
E.coli LPAAT	301	-SIMEQKIAE	LDKEVA-ER	EAAGKV*	-----
H.influenzae	301	TILMEKRIAE	LDEEIA	-----KGN*	-----
S.typhimuriu	301	TALMEQKIAE	LDKEVA-ER	EATGKV*	-----
L.douglassi	301	IYVRNLPASQ	KPLGS-TNR	-S-K*	-----
C. nucifera	301	TALYVDHLPE	SQKPLVSKGR	DASGRNS*	-----
	360	370	380	390	
Human LPAAT-β	351	-----	-----	-----	-----
Human LPAAT-α	351	-----	-----	-----	-----
Yeast LPAAT	351	SNDVNTNHNEG	SSVKKMH*	-----	-----
E.coli LPAAT	351	-----	-----	-----	-----
H.influenzae	351	-----	-----	-----	-----
S.typhimuriu	351	-----	-----	-----	-----
L.douglassi	351	-----	-----	-----	-----
C. nucifera	351	-----	-----	-----	-----

Figure 9 A

TCTATGAAACCAACATACATGGCGTTTGCATCACAGTTGGAGTCAGATGTGAGCCCGGAG	60
GGCAGGTGTCTGGCTTGTCCACCCGGAAGCCCTGAGGGCAGCTGTTCCCACTGGCTCTGC	120
TGACCTTGTGCCTTGGACGGCTGTCCTCAGCGAGGGGCGGTGCACCCGCTCCTGAGCAGC	180
GCC ATG GGC CTG CTG GCC TTC CTG AAG ACC CAG TTC GTG CTG CAC	225
Met Gly Leu Leu Ala Phe Leu Lys Thr Gln Phe Val Leu His	
5 10	
CTG CTG GTC GGC TTT GTC TTC GTG GTG AGT GGT CTG GTC ATC AAC	270
Leu Leu Val Gly Phe Val Phe Val Val Ser Gly Leu Val Ile Asn	
15 20 25	
TTC GTC CAG CTG TGC ACG CTG GCG CTC TGG CCG GTC AGC AAG CAG	315
Phe Val Gln Leu Cys Thr Leu Ala Leu Trp Pro Val Ser Lys Gln	
30 35 40	
CTC TAC CGC CGC CTC AAC TGC CGC CTC GCA TAC TCA CTC TGG AGC	360
Leu Tyr Arg Arg Leu Asn Cys Arg Leu Ala Tyr Ser Leu Trp Ser	
45 50 55	
CAA CTG GTC ATG CTG CTG GAG TGG TGG TCC TGC ACG GAG TGT ACA	405
Gln Leu Val Met Leu Leu Glu Trp Trp Ser Cys Thr Glu Cys Thr	
60 65 70	
CTG TTC ACG GAC CAG GCC ACG GTA GAG CGC TTT GGG AAG GAG CAC	450
Leu Phe Thr Asp Gln Ala Thr Val Glu Arg Phe Gly Lys Glu His	
75 80 85	
GCA GTC ATC ATC CTC AAC CAC AAC TTC GAG ATC GAC TTC CTC TGT	495
Ala Val Ile Ile Leu Asn His Asn Phe Glu Ile Asp Phe Leu Cys	
90 95 100	
GGG TGG ACC ATG TGT GAG CGC TTC GGA GTG CTG GGG AGC TCC AAG	540
Gly Trp Thr Met Cys Glu Arg Phe Gly Val Leu Gly Ser Ser Lys	
105 110 115	
GTC CTC GCT AAG AAG GAG CTG CTC TAC GTG CCC CTC ATC GGC TGG	585
Val Leu Ala Lys Lys Glu Leu Leu Tyr Val Pro Leu Ile Gly Trp	
120 125 130	
ACG TGG TAC TTT CTG GAG ATT GTG TTC TGC AAG CGG AAG TGG GAG	630
Thr Trp Tyr Phe Leu Glu Ile Val Phe Cys Lys Arg Lys Trp Glu	
135 140 145	
GAG GAC CGG GAC ACC GTG GTC GAA GGG CTG AGG CGC CTG TCG GAC	675
Glu Asp Arg Asp Thr Val Val Glu Gly Leu Arg Arg Leu Ser Asp	
150 155 160	
TAC CCC GAG TAC ATG TGG TTT CTC CTG TAC TGC GAG GGG ACG CGC	720
Tyr Pro Glu Tyr Met Trp Phe Leu Leu Tyr Cys Glu Gly Thr Arg	
165 170 175	
TTC ACG GAG ACC AAG CAC CGC GTT AGC ATG GAG GTG GCG GCT GCT	765
Phe Thr Glu Thr Lys His Arg Val Ser Met Glu Val Ala Ala Ala	
180 185 190	
AAG GGG CTT CCT GTC CTC AAG TAC CAC CTG CTG CCG CGG ACC AAG	810
Lys Gly Leu Pro Val Leu Lys Tyr His Leu Leu Pro Arg Thr Lys	
195 200 205	
GGC TTC ACC ACC GCA GTC AAG TGC CTC CGG GGG ACA GTC GCA GCT	855
Gly Phe Thr Thr Ala Val Lys Cys Leu Arg Gly Thr Val Ala Ala	
210 215 220	
GTC TAT GAT GTA ACC CTG AAC TTC AGA GGA AAC AAG AAC CCG TCC	900
Val Tyr Asp Val Thr Leu Asn Phe Arg Gly Asn Lys Asn Pro Ser	
225 230 235	
CTG CTG GGG ATC CTC TAC GGG AAG AAG TAC GAG GCG GAC ATG TGC	945
Leu Leu Gly Ile Leu Tyr Gly Lys Lys Tyr Glu Ala Asp Met Cys	
240 245 250	
GTG AGG AGA TTT CCT CTG GAA GAC ATC CCG CTG GAT GAA AAG GAA	990
Val Arg Arg Phe Pro Leu Glu Asp Ile Pro Leu Asp Glu Lys Glu	
255 260 265	
GCA GCT CAG TGG CTT CAT AAA CTG TAC CAG GAG AAG GAC GCG CTC	1035

Figure 10 A

CACGCTGGCGCTCTGGCCGGTCAGCAAGCAGCTCTACCGCCGCCTCAACTGCCGCCTCGCC	61
TACTCACTCTGGAGCCTAGCACAAAACCTAGAAGCAACCCAAGCACCTGTCACTGGAGACT	121
AATTATGCGGCACCCATACAGGGACCCCTCTGCGGCCATCATGGAGAGCCTTCATCTTGCC	181
CGTACAGTTTAAAGCGAAAAAGGAAGTATACAACAAAGTCCATAACTGGTC ATG CTG	238
	Met Leu
CTG GAG TGG TGG TCC TGC ACG GAG TGT ACA CTG TTC ACG GAC CAG	283
Leu Glu Trp Trp Ser Cys Thr Glu Cys Thr Leu Phe Thr Asp Gln	
5 10 15	
GCC ACG GTA GAG CGC TTT GGG AAG GAG CAC GCA GTC ATC ATC CTC	328
Ala Thr Val Glu Arg Phe Gly Lys Glu His Ala Val Ile Ile Leu	
20 25 30	
AAC CAC AAC TTC GAG ATC GAC TTC CTC TGT GGG TGG ACC ATG TGT	373
Asn His Asn Phe Glu Ile Asp Phe Leu Cys Gly Trp Thr Met Cys	
35 40 45	
GAG CGC TTC GGA GTG CTG GGG AGC TCC AAG GTC CTC GCT AAG AAG	418
Glu Arg Phe Gly Val Leu Gly Ser Ser Lys Val Leu Ala Lys Lys	
50 55 60	
GAG CTG CTC TAC GTG CCC CTC ATC GGC TGG ACG TGG TAC TTT CTG	463
Glu Leu Leu Tyr Val Pro Leu Ile Gly Trp Thr Trp Tyr Phe Leu	
65 70 75	
GAG ATT GTG TTC TGC AAG CGG AAG TGG GAG GAG GAC CGG GAC ACC	508
Glu Ile Val Phe Cys Lys Arg Lys Trp Glu Glu Asp Arg Asp Thr	
80 85 90	
GTG GTC GAA GGG CTG AGG CGC CTG TCG GAC TAC CCC GAG TAC ATG	553
Val Val Glu Gly Leu Arg Arg Leu Ser Asp Tyr Pro Glu Tyr Met	
95 100 105	
TGG TTT CTC CTG TAC TGC GAG GGG ACG CGC TTC ACG GAG ACC AAG	598
Trp Phe Leu Leu Tyr Cys Glu Gly Thr Arg Phe Thr Glu Thr Lys	
110 115 120	
CAC CGC GTT AGC ATG GAG GTG GCG GCT GCT AAG GGG CTT CCT GTC	643
His Arg Val Ser Met Glu Val Ala Ala Ala Lys Gly Leu Pro Val	
125 130 135	
CTC AAG TAC CAC CTG CTG CCG CGG ACC AAG GGC TTC ACC ACC GCA	688
Leu Lys Tyr His Leu Leu Pro Arg Thr Lys Gly Phe Thr Thr Ala	
140 145 150	
GTC AAG TGC CTC CGG GGG ACA GTC GCA GCT GTC TAT GAT GTA ACC	733
Val Lys Cys Leu Arg Gly Thr Val Ala Ala Val Tyr Asp Val Thr	
155 160 165	
CTG AAC TTC AGA GGA AAC AAG AAC CCG TCC CTG CTG GGG ATC CTC	778
Leu Asn Phe Arg Gly Asn Lys Asn Pro Ser Leu Leu Gly Ile Leu	
170 175 180	
TAC GGG AAG AAG TAC GAG GCG GAC ATG TGC GTG AGG AGA TTT CCT	823
Tyr Gly Lys Lys Tyr Glu Ala Asp Met Cys Val Arg Arg Phe Pro	
185 190 195	
CTG GAA GAC ATC CCG CTG GAT GAA AAG GAA GCA GCT CAG TGG CTT	868
Leu Glu Asp Ile Pro Leu Asp Glu Lys Glu Ala Ala Gln Trp Leu	
200 205 210	
CAT AAA CTG TAC CAG GAG AAG GAC GCG CTC CAG GAG ATA TAT AAT	913
His Lys Leu Tyr Gln Glu Lys Asp Ala Leu Gln Glu Ile Tyr Asn	
215 220 225	
CAG AAG GGC ATG TTT CCA GGG GAG CAG TTT AAG CCT GCC CGG AGG	958
Gln Lys Gly Met Phe Pro Gly Glu Gln Phe Lys Pro Ala Arg Arg	
230 235 240	
CCG TGG ACC CTC CTG AAC TTC CTG TCC TGG GCC ACC ATT CTC CTG	1003
Pro Trp Thr Leu Leu Asn Phe Leu Ser Trp Ala Thr Ile Leu Leu	
245 250 255	
TCT CCC CTC TTC AGT TTT GTC TTG GGC GTC TTT GCC AGC GGA TCA	1048
Ser Pro Leu Phe Ser Phe Val Leu Gly Val Phe Ala Ser Gly Ser	

Figure 10 B

	260		265		270		
CCT CTC CTG ATC CTG ACT TTC TTG GGG TTT GTG GGA GCA GCT TCC						1093	
Pro Leu Leu Ile Leu Thr Phe Leu Gly Phe Val Gly Ala Ala Ser							
	275		280		285		
TTT GGA GTT CGC AGA CTG ATA GGA GTA ACT GAG ATA GAA AAA GGC						1138	
Phe Gly Val Arg Arg Leu Ile Gly Val Thr Glu Ile Glu Lys Gly							
	290		295		300		
TCC AGC TAC GGA AAC CAA GAG TTT AAG AAA AAG GAA TAA TTAATGGC						1185	
Ser Ser Tyr Gly Asn Gln Glu Phe Lys Lys Lys Glu ***							
	305		310				
TGTGACTGAACACACGCGGCCCTGACGGTGGTATCCAGTTAACTCAAAACCAACACACAG						1245	
AGTGCAGGAAAAGACAATTAGAACTATTTTTCTTATTAAGTGGTGACTAATATTAACAA						1305	
AACTTGAGCCAAGAGTAAAGAATTCAGAAGGCCTGTGAGGTGAAGTCTTCAGCCTCCAC						1365	
AGCGCAGGGTCCCAGCATCTCCACGCGCGCCCGTGGGAGGTGGGTCCGGCCGGAGAGGCC						1425	
TCCCGCGGACGCGTCTCTCCAGAACTCCGCTTCCAAGAGGGACCTTTGGCTGCTTTCTC						1485	
TCCTTAAACTTAGATCAAATTTTAAAAAAAAAAAAAAAA						1523	

